



SEQUENCE LISTING

<110> Curtis, Rory A.J., Lora, Jose M.

<120> 46793, A Human Matrix Metalloprotease and
Uses Therefore

<130> MPI2001-014P1RNM

<140> 10/050,216

<141> 2002-01-16

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<151> 2001-01-16

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<211> 2310

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (317)...(1651)

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aaacccccggg acagtccttc tccgtgcggg ggcgggctag agcagtccca tccccggggt 240
ccggggcgcg gctgactgcc ggttggtccc ctgcgcgcag tagctccccg agccgggctg 300
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Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu
1 5 10

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cag ctg cta ctg tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga 400
Gln Leu Leu Leu Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly
15 20 25
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ggc cag gag ctg cgc aag gag gcg gag gca ttc cta gag aag tac gga 448
Gly Gln Glu Leu Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly
30 35 40
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tac ctc aat gaa cag gtc ccc aaa gct ccc acc tcc act cga ttc agc 496
Tyr Leu Asn Glu Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser
45 50 55 60
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gat gcc atc aga gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc 544
Asp Ala Ile Arg Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly
65 70 75
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gtg ttg gac cgc gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggc 592
Val Leu Asp Arg Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly
80 85 90
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gtt aca gat acc aac agt tat gcg gcc tgg gct gag agg atc agt gat 640
Val Thr Asp Thr Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp
95 100 105
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ttg ttt gct aga cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca 688
Leu Phe Ala Arg His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala
110 115 120
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aag caa ggg ggc gcc ctg gcg cac gcc ttc ctg ccc cgc cgc ggc gaa 736
Lys Gln Gly Gly Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu
125 130 135 140
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Ala His Phe Asp Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly
145 150 155
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agg aac atg ttc gtg gtg ctg ggc cac gag atc ggt cac acg att ggc	832
Arg Asn Leu Phe Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly	
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ctc acc cac tgc ccc ggc cag cgc gag ctc atg ggc ccc tac tac aag	880
Leu Thr His Ser Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys	
175 180 185	
agg ctg ggc cgc gac ggc ctg ctc agc tgg gac gac gtg ctg gcc gtg	928
Arg Leu Gly Arg Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val	
190 195 200	
cag agc ctg tat ggg aag ccc cta ggg ggc tca gtg gcc gta cag ctc	976
Gln Ser Leu Tyr Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu	
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cca gga aag ctg ttc act gac ttt gag acc tgg gac tcc tac agc ccc	1024
Pro Gly Lys Leu Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro	
225 230 235	
caa gga agg cgc cct gaa acg cag ggc cct aaa tac tgc cac tct tcc	1072
Gln Gly Arg Arg Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser	
240 245 250	
ttc gat gcc atc act gta gac agg caa cag caa ctg tac att ttt aaa	1120
Phe Asp Ala Ile Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys	
255 260 265	
ggg agc cat ttc tgg gag gtg gca gcc gat ggc aac gtc tca gag ccc	1168
Gly Ser His Phe Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro	
270 275 280	
cgt cca ctg cag gaa aga tgg gtc ggg ctg ccc ccc aac att gag gcc	1216
Arg Pro Leu Gln Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala	
285 290 295 300	
gcg gca gtg tca ttg aat gat gga gat ttc tac ttc ttc aaa ggg ggt	1264
Ala Ala Val Ser Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly	
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cga tgc tgg agg ttc cgg ggc ccc aag cca gtg tgg ggt ctc cca cag	1312
Arg Cys Trp Arg Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln	
320 325 330	
ctg tgc cgg gca ggg ggc ctg ccc cgc cat cct gac gcc gcc ctc ttc	1360
Leu Cys Arg Ala Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe	
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ttc cct cct ctg cgc cgc ctc atc ctc ttc aag ggt gcc cgc tac tac	1408
Phe Pro Pro Leu Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr	
350 355 360	
gtg ctg gcc cga ggg gga ctg caa gtg gag ccc tac tac ccc cga agt	1456
Val Leu Ala Arg Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser	
365 370 375 380	
ctg cag gac tgg gga ggc att cct gag gag gtc agc gcc gcc ctg ccg	1504
Leu Gln Asp Trp Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro	
385 390 395	
agg ccc gat ggc tcc atc atc ttc ttc cga gat gat cgc tac tgg cgc	1552
Arg Pro Asp Gly Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg	
400 405 410	
ctc gac cag gcc aaa ctg cag gca acc acc tgg ggc ccc tgg gcc acc	1600
Leu Asp Gln Ala Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr	
415 420 425	
gag ctg ccc tgg atg ggc tgc tgg cat gcc aac tgg ggg agc gcc ctg	1648
Glu Leu Pro Trp Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu	
430 435 440	
ttc tgaaggcacc tctcaccctc agaaactggt ggtgctctca gggcaaaatc	1701
Phe	
445	
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cggggcagca aagcctccat ctggaagtct gtctgccttt gttccttgaa gaatgcagca 1321
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tcaggacaca gattgggagg gagaactgat caggcctacc agtcctctgc tttttgtctg 2241
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 <212> PRT
 <213> Homo sapiens

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Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu
 35     40     45
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg
 50     55     60
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg
 65     70     75     80
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr
 85     90     95
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg
100    105    110
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly
115    120    125
Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp
130    135    140
Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe
145    150    155    160
Val Val Leu Ala His Gly Ile Gly His Thr Leu Gly Leu Thr His Ser
165    170    175
Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg
180    185    190
Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr
195    200    205
Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu
210    215    220
Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg
225    230    235
Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile
245    250    255
Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe
260    265    270
Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln
275    280    285
Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala Ala Val Ser
290    295    300
Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg
305    310    315
Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala
325    330    335
Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu
340    345    350
Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg
355    360    365
Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp
370    375    380
Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly
385    390    395
Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala
405    410    415
Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp
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Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu Phe
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<212> DNA
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tgg ggc cac ctg gac gcc cag ccc gcc gag cgc gga ggc cag gag ctg 96
Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu
20 25 30

cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa 144
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu
35 40 45

cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga 192
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg
50 55 60

gcc ttt cag tgg gtg tcc cag cta cct gtc agc gcc gtg ttg gac cgc 240
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg
65 70 75 80

gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc 288
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr
85 90 95

aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga 336
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg
100 105 110

cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggg gcc 384
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly
115 120 125

gcc ctg gcg cac gcc ttc ctg ccc cgc cgc gcc gaa gcc cac ttc gac 432
Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp
130 135 140

caa gat gag cgc tgg tcc ctg agc cgc cgc cgc ggg cgc aac ctg ttc 480
Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe
145 150 155 160

gtg gtg ctg gcg cac gag atc ggt cac acg ctt gcc ctc acc cac tgc 528
Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly Leu Thr His Ser
165 170 175

ccc gcg ccg cgc gcg ctc atg gcg ccc tac tac aag agg ctg gcc cgc 576
Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg
180 185 190

gac gcg ctg ctc agc tgg gac gac gtg ctg gcc gtg cag agc ctg tat 624
Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr
195 200 205

ggg aag ccc cta ggg gcc tca gtg gcc gtc cag ctc cca gga aag ctg 672
Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu
210 215 220

ttc act gac ttt gag acc tgg gac tcc tac agc ccc caa gga agg cgc 720
Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg
225 230 235 240

cct gaa acg cag gcc cct aaa tac tgc cac tct tcc ttc gat gcc atc 768
Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile
245 250 255

act gta gac agg caa cag caa ctg tac att ttt aaa ggg agc cat ttc 816
Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe
260 265 270

tgg gag gtg gca gct gat gcc aac gtc tca gag ccc cgt cca ctg cag 864

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Trp	Glu	Val	Ala	Ala	Asp	Gly	Asn	Val	Ser	Glu	Pro	Arg	Pro	Leu	Gln		
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Glu	Arg	Trp	Val	Gly	Leu	Pro	Pro	Asn	Ile	Glu	Ala	Ala	Ala	Val	Ser		
		290				295				300							
ttg	aat	gat	gga	gat	ttc	tac	ttc	ttc	aaa	ggg	ggt	cga	tgc	tgg	agg	960	
Leu	Asn	Asp	Gly	Asp	Phe	Tyr	Phe	Phe	Lys	Gly	Gly	Arg	Cys	Trp	Arg		
		305			310				315						320		
ttc	egg	ggc	ccc	aag	cca	gtg	tgg	ggt	ctc	cca	cag	ctg	tgc	egg	gca	1008	
Phe	Arg	Gly	Pro	Lys	Pro	Val	Trp	Gly	Leu	Pro	Gln	Leu	Cys	Arg	Ala		
			325					330						335			
ggg	ggc	ctg	ccc	egg	cat	cat	gac	gcc	gcc	ctc	ttc	ttc	ccc	ccc	ctg	1056	
Gly	Gly	Leu	Pro	Arg	His	Pro	Asp	Ala	Ala	Leu	Phe	Phe	Pro	Pro	Leu		
		340					345						350				
ggc	ggc	ctc	atc	ctc	ttc	aag	ggt	gcc	ggc	tac	tac	gtg	ctg	gcc	cga	1104	
Arg	Arg	Leu	Ile	Leu	Phe	Lys	Gly	Ala	Arg	Tyr	Tyr	Val	Leu	Ala	Arg		
		355				360						365					
ggg	gga	ctg	caa	gtg	gag	ccc	tac	tac	ccc	cga	agt	ctg	cag	gac	tgg	1152	
Gly	Gly	Leu	Gln	Val	Glu	Pro	Tyr	Tyr	Pro	Arg	Ser	Leu	Gln	Asp	Trp		
		370			375						380						
gga	ggc	atc	ccc	gag	gag	gtc	agc	ggc	gcc	ctg	ccg	agg	ccc	gat	ggc	1200	
Gly	Gly	Ile	Pro	Glu	Glu	Val	Ser	Gly	Ala	Leu	Pro	Arg	Pro	Asp	Gly		
		385			390					395				400			
ttc	atc	atc	ttc	ttc	cga	gat	gac	ggc	tac	tgg	ggc	ctc	gac	cag	gcc	1248	
Ser	Ile	Ile	Phe	Phe	Arg	Asp	Asp	Arg	Tyr	Trp	Arg	Leu	Asp	Gln	Ala		
			405					410						415			
aaa	ctg	cag	gca	acc	acc	tgg	ggc	ggc	tgg	gcc	acc	gag	ctg	ccc	tgg	1296	
Lys	Leu	Gln	Ala	Thr	Thr	Ser	Gly	Arg	Trp	Ala	Thr	Glu	Leu	Pro	Trp		
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atg	ggc	tgc	tgg	cat	gcc	aac	tgg	ggg	agg	ggc	ctg	ttc				1336	
Met	Gly	Cys	Trp	His	Ala	Asn	Ser	Gly	Ser	Ala	Leu	Phe					
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 <313> Artificial Sequence

<320>
 <323> Consensus

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Thr	Arg	Lys	Lys	Ala	Ser	Asn	Ser	Leu	Val	Glu	Lys	Leu	Lys	Glu	Met		
			20				25						30				
Gln	Lys	Phe	Phe	Gly	Leu	Pro	Val	Thr	Gly	Lys	Leu	Asp	Ser	Asn	Thr		
		35				40						45					
Leu	Glu	Val	Met	Lys	Lys	Pro	Arg	Cys	Gly	Val	Pro	Asp	Val	Gly	Glu		
	50				55					60							
Phe	Arg	Thr	Phe	Pro	Gly	Ser	Pro	Lys	Trp	Ser	Lys	Asn	Asn	Leu	Leu		
	65			70					75					80			
Thr	Tyr	Arg	Ile	Val	Asn	Tyr	Thr	Pro	Asp	Leu	Pro	Arg	Glu	Asp	Val		
			85					90					95				
Asp	Asp	Ala	Ile	Arg	Arg	Ala	Phe	Gln	Val	Trp	Ser	Asp	Val	Thr	Pro		
	100					105							110				
Leu	Thr	Phe	Thr	Arg	Val	Ser	Asp	Gly	Glu	Ala	Asp	Ile	Met	Ile	Ser		
	115				120							125					
Phe	Ala	Arg	Gly	Glu	His	Gly	Asp	Phe	Tyr	Pro	Phe	Asp	Gly	Lys	Gly		
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Gly	Leu	Leu	Ala	His	Ala	Phe	Ala	Pro	Gly	Pro	Gly	Ile	Gly	Ile	Gly		
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus

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 Asp Pro Gly Tyr Pro Lys Leu Ile Ser Asp Leu Trp Pro Asp Gly Leu
 35 40 45
 Pro Cys
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<210> 6
 <211> 471
 <212> PRT
 <213> Homo sapiens

<400> 6
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 1 5 10 15
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 20 25 30
 Glu Glu Asp Leu Gln Phe Ala Glu Arg Tyr Leu Arg Ser Tyr Tyr His
 35 40 45
 Pro Thr Asn Leu Ala Gly Ile Leu Lys Glu Asn Ala Ala Ser Ser Met
 50 55 60
 Thr Glu Arg Leu Arg Glu Met Gln Ser Phe Phe Gly Leu Glu Val Thr
 65 70 75 80
 Gly Lys Leu Asp Asp Asn Thr Leu Asp Val Met Lys Lys Pro Arg Cys
 85 90 95
 Gly Val Pro Asp Val Gly Glu Tyr Asn Val Phe Pro Arg Thr Leu Lys
 100 105 110
 Trp Ser Lys Met Asn Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp
 115 120 125
 Met Thr His Ser Glu Val Glu Lys Ala Phe Lys Lys Ala Phe Lys Val
 130 135 140
 Trp Ser Asp Val Thr Pro Leu Asn Phe Thr Arg Leu His Asp Gly Ile
 145 150 155 160
 Ala Asp Ile Met Ile Ser Phe Gly Ile Lys Glu His Gly Asp Phe Tyr
 165 170 175
 Pro Phe Asp Gly Pro Ser Gly Leu Leu Ala His Ala Phe Pro Pro Gly
 180 185 190
 Pro Asn Tyr Gly Gly Asp Ala His Phe Asp Asp Asp Glu Thr Trp Thr
 195 200 205
 Ser Ser Ser Lys Gly Tyr Asn Leu Phe Leu Val Ala Ala His Glu Phe
 210 215 220
 Gly His Ser Leu Gly Leu Asp His Ser Lys Asp Pro Gly Ala Leu Met
 225 230 235 240
 Phe Pro Ile Tyr Thr Tyr Thr Gly Lys Ser His Phe Met Leu Pro Asp
 245 250 255
 Asp Asp Val Gln Gly Ile Gln Ser Leu Tyr Gly Pro Gly Asp Glu Asp
 260 265 270
 Pro Asn Pro Lys His Pro Lys Thr Pro Asp Lys Cys Asp Pro Ser Leu
 275 280 285
 Ser Leu Asp Ala Ile Thr Ser Leu Arg Gly Glu Thr Met Ile Phe Lys
 290 295 300
 Asp Arg Phe Phe Trp Arg Leu His Pro Gln Gln Val Asp Ala Glu Leu
 305 310 315 320
 Phe Leu Thr Lys Ser Phe Trp Pro Glu Leu Pro Asn Arg Ile Asp Ala
 325 330 335
 Ala Tyr Glu His Pro Ser His Asp Leu Ile Phe Ile Phe Arg Gly Arg
 340 345 350
 Lys Phe Trp Ala Leu Asn Gly Tyr Asp Ile Leu Glu Gly Tyr Pro Lys
 355 360 365
 Lys Ile Ser Glu Leu Gly Leu Pro Lys Glu Val Lys Lys Ile Ser Ala
 370 375 380
 Ala Val His Phe Glu Asp Thr Gly Lys Thr Leu Leu Phe Ser Gly Asn
 385 390 395 400
 Gln Val Trp Arg Tyr Asp Asp Thr Asn His Ile Met Asp Lys Asp Tyr
 405 410 415

Pro Arg Leu Ile Glu Glu Asp Phe Pro Gly Ile Gly Asp Lys Val Asp
 420 425 430
 Ala Val Tyr Glu Lys Asn Gly Tyr Ile Tyr Phe Phe Asn Gly Pro Ile
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 Gln Phe Glu Tyr Ser Ile Trp Ser Asn Arg Ile Val Arg Val Met Pro
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 Ala Asn Ser Ile Leu Trp Cys
 465 470

<210> 7
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus

<231> VARIANT
 <232> (1)...(1)
 <233> Xaa = G, S, T, A, L, I, V, or N.

<231> VARIANT
 <232> (2)...(2)
 <233> Xaa at position 2 = A, E, Q, D, N, L, G, K, S, V, R, T, P, I,
 M, F, Y, C, W, or H.

<231> VARIANT
 <232> (3)...(3)
 <233> Xaa at position 3 = A, E, Q, D, N, L, G, K, S, V, R, T, P, I,
 M, F, Y, C, W, or H.

<231> VARIANT
 <232> (6)...(6)
 <233> Xaa at position 6 = L, I, V, M, Y, or W.

<231> VARIANT
 <232> (7)...(7)
 <233> Xaa at position 7 = A, Q, N, L, G, S, V, T, I, M, F, Y, C, or W.

<231> VARIANT
 <232> (9)...(9)
 <233> Xaa at position 9 = A, E, Q, D, N, L, G, K, S, V, R, T, P, I,
 M, F, Y, C, W, or H.

<231> VARIANT
 <232> (10)...(10)
 <233> Xaa at position 10 = L, I, V, M, F, Y, W, G, S, P, or Q.

<400> 7
 Xaa Xaa Xaa His Glu Xaa Xaa His Xaa Xaa
 1 5 10

<210> 8
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<220>
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 <222> (300)...(1959)

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 ccaggcgagg agcgccccag agcggcgcgc tagggcactg gcgaaacccc gggacagtc 180
 ccttcctgtc gggggggggc cagagcagtc ccatcccccgg ggtccggggc ggggtcga 240
 ggcggctgggt tccctggcg cagtagctcc ccgagccggg ctgcacccga ggcggcgag 299
 atg gtc ggc cgc gtc ggc ctc ctg ctg cgc gcc ctg cag ctg cta ctg 347
 Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu Gln Leu Leu Leu
 1 5 10 15

tgg ggc cac ctg gac gcc cag ccc ggc gag cgc gga ggc cag gag ctg 395
 Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu

20	25	30	
cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu 35 40 45			443
cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg 50 55 60			491
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gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr 85 90 95			587
aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga Asn Ser Tyr Thr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg 100 105 110			635
cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggt aac His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Gln Gly Asn 115 120 125			683
aaa tgg tac aag cag cac ctc tcc tac cgc ctg gtg aac tgg cct gag Lys Trp Tyr Lys Gln His Leu Ser Tyr Arg Leu Val Asn Trp Pro Glu 130 135 140			731
cat ctg ccg gag ccg gca gtt cgg ggc gcc gtg cgc gcc gcc ttc cag His Leu Pro Glu Pro Ala Val Arg Gly Ala Val Arg Ala Ala Phe Gln 145 150 155 160			779
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ggc ccc gct gac atc cgg ctc acc ttc ttc caa ggg gac cac aac gat Gly Pro Ala Asp Ile Arg Leu Thr Phe Phe Gln Gly Asp His Asn Asp 180 185 190			875
ggg ctg ggc aat gcc ttt gat ggc cca ggg ggc gcc ctg gcg cac gcc Gly Leu Gly Asn Ala Phe Asp Gly Pro Gly Gly Ala Leu Ala His Ala 195 200 205			923
ttc ctg ccc cgc cgc ggc gaa gcg cac ttc gac caa gat gag cgc tgg Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp Gln Asp Glu Arg Trp 210 215 220			971
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gag atc ggt cac acg ctt ggc ctc acc cac tcc ccc gcg ccg cgc gcg Glu Ile Gly His Thr Leu Gly Leu Thr His Ser Pro Ala Pro Arg Ala 245 250 255			1067
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ggc tca gtg gcc gtc cag ctc cca gga aag ctg ttc act gac ttt gag Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu Phe Thr Asp Phe Glu 290 295 300			1211
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 Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln Glu Arg Trp Val Gly
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 ctg ccc ccc aac att gag gct ggg gca gtg tca ttg aat gat gga gat 1481
 Leu Pro Pro Asn Ile Glu Ala Ala Val Ser Leu Asn Asp Gly Asp
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 Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg Phe Arg Gly Pro Lys
 385 390 395 400
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 Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala Gly Gly Leu Pro Arg
 405 410 415
 cat cct gac gcc gcc ctc ttc ttc cct cct ctg cgc cgc ctc atc ctc 1595
 His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu Arg Arg Leu Ile Leu
 420 425 430
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 Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg Gly Gly Leu Gln Val
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 Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp Gly Gly Ile Pro Glu
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 Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly Ser Ile Ile Phe Phe
 465 470 475 480
 cga gat gac cgc tac tgg cgc ctc gac cag gcc aaa ctg cag gca acc 1787
 Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala Lys Leu Gln Ala Thr
 485 490 495
 acc tcc ggc cgc tgg gcc acc gag ctg ccc tgg atg ggc tgc tgg cat 1835
 Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp Met Gly Cys Trp His
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 gcc aac tcc ggg agc gcc ctg ttc tgaaggacc tctcaccctc agaaactggt 1889
 Ala Asn Ser Gly Ser Ala Leu Phe
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 Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu
 35 40 45
 Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg
 50 55 60
 Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg
 65 70 75 80

Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr
 85 90 95
 Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg
 100 105 110
 His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Asn
 115 120 125
 Lys Trp Tyr Lys Gln His Leu Ser Tyr Arg Leu Val Asn Trp Pro Glu
 130 135 140
 His Leu Pro Glu Pro Ala Val Arg Gly Ala Val Arg Ala Ala Phe Gln
 145 150 155 160
 Leu Trp Ser Asn Val Ser Ala Leu Glu Phe Trp Glu Ala Pro Ala Thr
 165 170 175
 Gly Pro Ala Asp Ile Arg Leu Thr Phe Phe Gln Gly Asp His Asn Asp
 180 185 190
 Gly Leu Gly Asn Ala Phe Asp Gly Pro Gly Gly Ala Leu Ala His Ala
 195 200 205
 Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp Gln Asp Glu Arg Trp
 210 215 220
 Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe Val Val Leu Ala His
 225 230 235 240
 Glu Ile Gly His Thr Leu Gly Leu Thr His Ser Pro Ala Pro Arg Ala
 245 250 255
 Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg Asp Ala Leu Leu Ser
 260 265 270
 Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr Gly Lys Pro Leu Gly
 275 280 285
 Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu Phe Thr Asp Phe Glu
 290 295 300
 Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg Pro Glu Thr Gln Gly
 305 310 315 320
 Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile Thr Val Asp Arg Gln
 325 330 335
 Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe Trp Glu Val Ala Ala
 340 345 350
 Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln Glu Arg Trp Val Gly
 355 360 365
 Leu Pro Pro Asn Ile Glu Ala Ala Val Ser Leu Asn Asp Gly Asp
 370 375 380
 Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg Phe Arg Gly Pro Lys
 385 390 395 400
 Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala Gly Gly Leu Pro Arg
 405 410 415
 His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu Arg Arg Leu Ile Leu
 420 425 430
 Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg Gly Gly Leu Gln Val
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 450 455 460
 Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly Ser Ile Ile Phe Phe
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 tgg gcc cac ctg gac gcc cag ccc gcg gag cgc gga gcc cag gag ctg 96
 Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu
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 cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa 144

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cag	gtc	ccc	aaa	gct	ccc	acc	tcg	act	cga	ttc	agg	gat	gcc	atc	aga	192	
Gln	Val	Pro	Lys	Ala	Pro	Thr	Ser	Thr	Arg	Phe	Ser	Asp	Ala	Ile	Arg		
	50					55					60						
ggg	ttt	cag	tgg	gtg	tcc	cag	cta	cct	gtc	agg	ggc	gtg	ttg	gac	cgc	240	
Ala	Phe	Gln	Trp	Val	Ser	Gln	Leu	Pro	Val	Ser	Gly	Val	Leu	Asp	Arg		
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gcc	acc	ctg	cgc	cag	atg	act	cgt	ccc	cgc	tgc	ggg	gtt	aca	gat	acc	288	
Ala	Thr	Leu	Arg	Gln	Met	Thr	Arg	Pro	Arg	Cys	Gly	Val	Thr	Asp	Thr		
				85				90						95			
aac	agt	tat	ggg	gcc	tgg	gct	gag	agg	atc	agt	gac	ttg	ttt	gct	aga	336	
Asn	Ser	Tyr	Ala	Ala	Trp	Ala	Glu	Arg	Ile	Ser	Asp	Leu	Phe	Ala	Arg		
			100					105					110				
cac	cgg	acc	aaa	atg	agg	cgt	aag	aaa	cgc	ttt	gca	aag	caa	ggt	aac	384	
His	Arg	Thr	Lys	Met	Arg	Arg	Lys	Lys	Arg	Phe	Ala	Lys	Gln	Gly	Asn		
	115						120					125					
aaa	tgg	tac	aag	cag	cac	ctc	tcc	tac	cgc	ctg	gtg	aac	tgg	cct	gag	432	
Lys	Trp	Tyr	Lys	Gln	His	Leu	Ser	Tyr	Arg	Leu	Val	Asn	Trp	Pro	Glu		
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cat	ctg	cgg	gag	cgg	gca	gtt	cgg	ggc	gcc	gtg	cgc	gcc	gcc	ttc	cag	480	
His	Leu	Pro	Glu	Pro	Ala	Val	Arg	Gly	Ala	Val	Arg	Ala	Ala	Phe	Gln		
	145				150					155					160		
ttg	tgg	agg	aac	gtc	tca	ggg	ctg	gag	ttc	tgg	gag	gcc	cca	gcc	aca	528	
Leu	Trp	Ser	Asn	Val	Ser	Ala	Leu	Glu	Phe	Trp	Glu	Ala	Pro	Ala	Thr		
				165					170					175			
ggc	ccc	gct	gac	atc	cgg	ctc	acc	ttc	ttc	caa	ggg	gac	cac	aac	gat	576	
Gly	Pro	Ala	Asp	Ile	Arg	Leu	Thr	Phe	Phe	Gln	Gly	Asp	His	Asn	Asp		
			180					185					190				
ggg	ctg	ggg	aat	gcc	ttt	gat	ggc	cca	ggg	ggc	ggc	ctg	ggg	cac	ggc	624	
Gly	Leu	Gly	Asn	Ala	Phe	Asp	Gly	Pro	Gly	Gly	Ala	Leu	Ala	His	Ala		
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ttc	ctg	ccc	cgc	cgc	ggc	gaa	ggg	cac	ttc	gac	caa	gat	gag	cgc	tgg	672	
Phe	Leu	Pro	Arg	Arg	Gly	Glu	Ala	His	Phe	Asp	Gln	Asp	Glu	Arg	Trp		
	210					215					220						
tcc	ctg	agg	cgc	cgc	cgc	ggg	cgc	aac	ctg	ttc	gtg	gtg	ctg	ggg	cac	720	
Ser	Leu	Ser	Arg	Arg	Arg	Gly	Arg	Asn	Leu	Phe	Val	Val	Leu	Ala	His		
	225					230					235				240		
gag	atc	ggg	cac	agg	ctt	ggc	ctc	acc	cac	tgg	ccc	ggg	cgg	cgc	ggg	768	
Glu	Ile	Gly	His	Thr	Leu	Gly	Leu	Thr	His	Ser	Pro	Ala	Pro	Arg	Ala		
			245					250						255			
ctc	atg	ggg	ccc	tac	tac	aag	agg	ctg	ggc	cgc	gac	ggg	ctg	ctc	agg	816	
Leu	Met	Ala	Pro	Tyr	Tyr	Lys	Arg	Leu	Gly	Arg	Asp	Ala	Leu	Leu	Ser		
			260					265					270				
tgg	gac	gag	gtg	ctg	ggc	gtg	cag	agg	ctg	tat	ggg	aag	ccc	cta	ggg	864	
Trp	Asp	Asp	Val	Leu	Ala	Val	Gln	Ser	Leu	Tyr	Gly	Lys	Pro	Leu	Gly		
	275					280						285					
ggc	tca	gtg	ggc	gtc	cag	ctc	cca	gga	aag	ctg	ttc	act	gac	ttt	gag	912	
Gly	Ser	Val	Ala	Val	Gln	Leu	Pro	Gly	Lys	Leu	Phe	Thr	Asp	Phe	Glu		
	290					295					300						
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Thr	Trp	Asp	Ser	Tyr	Ser	Pro	Gln	Gly	Arg	Arg	Pro	Glu	Thr	Gln	Gly		
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cct	aaa	tac	tgc	cac	tct	tcc	ttc	gat	gcc	atc	act	gta	gac	agg	caa	1008	
Pro	Lys	Tyr	Cys	His	Ser	Ser	Phe	Asp	Ala	Ile	Thr	Val	Asp	Arg	Gln		
				325				330						335			
cag	caa	ctg	tac	att	ttt	aaa	ggg	agg	cat	ttc	tgg	gag	gtg	gca	gct	1056	
Gln	Gln	Leu	Tyr	Ile	Phe	Lys	Gly	Ser	His	Phe	Trp	Glu	Val	Ala	Ala		

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ctg ccc ccc aac att gag gct gcg gca gtg tca ttg aat gat gga gat Leu Pro Pro Asn Ile Glu Ala Ala Val Ser Leu Asn Asp Gly Asp 370 375 380			1152
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gag gtc agc ggc gcc ctg ccg agg ccc gat ggc tcc atc atc ttc ttc Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly Ser Ile Ile Phe Phe 465 470 475 480			1440
cga gat gac cgc tac tgg cgc ctc gac cag gcc aaa ctg cag gca acc Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala Lys Leu Gln Ala Thr 485 490 495			1488
acc tcg ggc cgc tgg gcc acc gag ctg ccc tgg atg ggc tgc tgg cat Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp Met Gly Cys Trp His 500 505 510			1536
gcc aac tcg ggg agc gcc ctg ttc tga Ala Asn Ser Gly Ser Ala Leu Phe * 515 520			1563